

## SEQUENCE LISTING

&lt;110&gt; SmithKline Beecham Biologicals S.A.

&lt;120&gt; Novel Compounds

&lt;130&gt; BM45412

&lt;160&gt; 10

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 1509

&lt;212&gt; DNA

<213> *Moraxella catarrhalis*

&lt;400&gt; 1

atgtctaagc	ctactttgat	aaaaacaacc	ttaatttgtg	ccttaagtgc	attgatgctc	60
agtgggtgta	gcaatcaagc	ggacaaaagc	gcccagccaa	aaagcagcac	ggtagacgct	120
gccgccaaga	cagcaaatgc	agataatgct	gcctcacaa	aacatcaagg	cgagctgcct	180
gtcattgatg	ccattgttac	gcatgcacca	gaagttccac	cacctgttga	ccgtgaccac	240
cccgcctaaag	tggtggtaaa	aatggaaacc	gttgaaaaag	tcatgcgtct	ggcagatggc	300
gtggaatata	agttttggac	atgtggcggg	caagttccag	ggcagatgat	tcgtgtgcgt	360
gaaggcgaca	ccatcgaagt	gcagttctca	aaccaccag	attcaaaaat	gccccataat	420
gttgactttc	acgctgccac	agggcctggc	ggcggggcag	aagcgtcatt	taccgcaccg	480
ggtcatacat	caacctttag	ttttaaaagc	ttacagcctg	gtttgtatgt	ctatcactgt	540
gcgggttgccc	ctgttggcat	gcacattgct	aatggcatgt	atgggtttgat	tttgggtgaa	600
ccaaaagagg	gcttgccaaa	agtagataaa	gaatactatg	tcatgcaagg	cgacttttat	660
accaaaggca	aatatggcga	acaagggtcta	cagccctttg	atatggaaaa	agccattcga	720
gaagatgctg	aatatgttgt	ctttaatggg	tcgggtgggg	cgttgactgg	tgaaaatgct	780
ctaaaagcca	aggttggcga	aactgttcgc	ttatttggg	gtaacggcgg	ccgaatttg	840
acatcatcat	tccatgtcat	tggtgagatt	tttgataagg	ttcactttga	gggtggtaag	900
ggtgaaaacc	acaatatcca	aaccacgcta	atcccagcag	gtggcgctgc	catcactgaa	960
tttaaggtgg	atgtgccggg	tgattatgtc	ttgggtgacc	atgccatctt	ccgtgccttt	1020
aacaaagggg	cattgggcat	acttaagggtg	gaagggtgaag	aaaatcatga	gattttattca	1080
cacaaacaaa	cagacgctgt	ctatctgcca	gagggtgccc	cacaagcaat	tgatacccaa	1140
gaagcaccca	aaacacctgc	acctgccaac	ttacaagagc	agattaaagc	aggtaaggca	1200
acctatgact	ctaactgtgc	tgcttgtcac	caacctgatg	gtaaaggcgt	gccaaacgct	1260
ttcccaccgc	ttgccaaactc	tgactatctg	aacgccgacc	acgctcgtgc	cgccagcatc	1320
gtggcaaatg	gattgtctgg	taagattacc	gtcaatggca	accaatatga	aagcgtcatg	1380
cctgcgattg	ctctgagcga	ccaacagatt	gccaatgtca	tcacctacac	gcttaacagc	1440
tttggttaaca	aaggcgggtca	actcagtgc	gacgatgtgg	caaaagccaa	aaaaaccaag	1500
ccaaactga						1509

&lt;210&gt; 2

&lt;211&gt; 502

&lt;212&gt; PRT

<213> *Moraxella catarrhalis*

&lt;400&gt; 2

Met	Ser	Lys	Pro	Thr	Leu	Ile	Lys	Thr	Thr	Leu	Ile	Cys	Ala	Leu	Ser
1				5				10				15			
Ala	Leu	Met	Leu	Ser	Gly	Cys	Ser	Asn	Gln	Ala	Asp	Lys	Ala	Ala	Gln
		20					25					30			
Pro	Lys	Ser	Ser	Thr	Val	Asp	Ala	Ala	Lys	Thr	Ala	Asn	Ala	Asp	

2

WO 01/19996

PCT/EP00/09035

500

<210> 3  
 <211> 1506  
 <212> DNA  
 <213> *Moraxella catarrhalis*

<400> 3  
 atgtctaagc ctactttgat aaaaacaacc ttaattttgtg ccttaagtgc attgatgctc 60  
 agtgggttgta gcaatcaagc ggacaaagcc gccagccaa aaagcagcac ggtagacgct 120  
 gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct 180  
 gtcattgatg ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac 240  
 cccgccaag tggtggtaaa aatggaaacc gttgaaaaag tcatgctgtc ggcagatggc 300  
 gtggaatata agttttggac atttggcggc caagttccag ggcagatgat tcgtgtgctc 360  
 gaaggcgaca ccatcgaagt gcagttctca aaccaccag attcaaaaat gccccataat 420  
 gttgactttc acgctgccac agggcctggc ggcggggcag aagcgtcatt taccgcaccg 480  
 ggtcatatat caacctttag ttttaaagcc ttacagcctg gtttgtatgt ctatcactgt 540  
 gcggttgccc ctggtggcat gcacattgct aatggcatgt atgggttgat tttggttgaa 600  
 ccaaaagagg gcttgccaaa agtagataaa gaatactatg tcatgcaagg cgacttttat 660  
 accaaaggca aatatggcga acaaggtcta cagccctttg atatggaaaa agccattcga 720  
 gaagatgctg aatatgttgt ctttaatggt tcggtggggg cgttgactgg tgaaaatgct 780  
 ctaaaagcca aggttggcga aactgttcgc ttatttgttg gtaacggcgg ccggaatttg 840  
 acatcatcat tccatgtcat tgggtgagatt tttgataagg ttcaacttga ggggtgtaag 900  
 ggtgaaaacc acaatatcca aaccacgcta atcccagcag gtggcgctgc catcactgaa 960  
 tttaagggtg atgtgccggg tgattatgtc ttggttgacc atgccatctt ccgtgccttt 1020  
 aacaaagggg cattgggcat acttaagggtg gaagggtgaag aaaatcatga gatttattca 1080  
 cacaacaaaa cagacgctgt ctatctgcca gaggggtgcc cacaagcaat tgatacccaa 1140  
 gaagcaccca aaacacctgc acctgccaac ttacaagagc agattaaagc aggtaaggca 1200  
 acctatgact ctaactgtgc tgcttgtcac caacctgatg gtaaaggcgt gccaaacgct 1260  
 ttcccaccgc ttgccaactc tgactatctg aacgccgacc acgctcgtgc cgccagcatc 1320  
 gtggcaaatg gattgtctgg taagattacc gtcaatggca accaatatga aagcgtcatg 1380  
 cctgcgattg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc 1440  
 tttggttaaca aaggcgggtca actcagtgc gacgatgtgg caaaagccaa aaaaaccaag 1500  
 ccaaac 1506

<210> 4  
 <211> 502  
 <212> PRT  
 <213> *Moraxella catarrhalis*

<400> 4  
 Met Ser Lys Pro Thr Leu Ile Lys Thr Thr Leu Ile Cys Ala Leu Ser  
 1 5 10 15  
 Ala Leu Met Leu Ser Gly Cys Ser Asn Gln Ala Asp Lys Ala Ala Gln  
 20 25 30  
 Pro Lys Ser Ser Thr Val Asp Ala Ala Lys Thr Ala Asn Ala Asp  
 35 40 45  
 Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala  
 50 55 60  
 Ile Val Thr His Ala Pro Glu Val Pro Pro Pro Val Asp Arg Asp His  
 65 70 75 80  
 Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg  
 85 90 95  
 Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val  
 100 105 110  
 Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln  
 115 120 125  
 Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His

130		135		140
Ala Ala Thr Gly Pro Gly	Gly Gly Ala Glu Ala	Ser Phe Thr Ala Pro		
145	150	155	160	
Gly His Thr Ser Thr Ph	Ser Phe Lys Ala Leu	Gln Pro Gly Leu Tyr		
	165	170	175	
Val Tyr His Cys Ala Val	Ala Pro Val Gly Met	His Ile Ala Asn Gly		
	180	185	190	
Met Tyr Gly Leu Ile Leu	Val Glu Pro Lys Glu Gly	Leu Pro Lys Val		
	195	200	205	
Asp Lys Glu Tyr Tyr Val	Met Gln Gly Asp Phe Tyr	Thr Lys Gly Lys		
	210	215	220	
Tyr Gly Glu Gln Gly Leu	Gln Pro Phe Asp Met Glu	Lys Ala Ile Arg		
225	230	235	240	
Glu Asp Ala Glu Tyr Val	Val Phe Asn Gly Ser Val	Gly Ala Leu Thr		
	245	250	255	
Gly Glu Asn Ala Leu Lys	Ala Lys Val Gly Glu Thr	Val Arg Leu Phe		
	260	265	270	
Val Gly Asn Gly Gly Pro	Asn Leu Thr Ser Ser Phe	His Val Ile Gly		
	275	280	285	
Glu Ile Phe Asp Lys Val	His Phe Glu Gly Gly Lys	Gly Glu Asn His		
	290	295	300	
Asn Ile Gln Thr Thr Leu	Ile Pro Ala Gly Gly Ala	Ala Ile Thr Glu		
305	310	315	320	
Phe Lys Val Asp Val Pro	Gly Asp Tyr Val Leu Val	Asp His Ala Ile		
	325	330	335	
Phe Arg Ala Phe Asn Lys	Gly Ala Leu Gly Ile Leu	Lys Val Glu Gly		
	340	345	350	
Glu Glu Asn His Glu Ile	Tyr Ser His Lys Gln Thr	Asp Ala Val Tyr		
	355	360	365	
Leu Pro Glu Gly Ala Pro	Gln Ala Ile Asp Thr Gln	Glu Ala Pro Lys		
	370	375	380	
Thr Pro Ala Pro Ala Asn	Leu Gln Glu Gln Ile Lys	Ala Gly Lys Ala		
385	390	395	400	
Thr Tyr Asp Ser Asn Cys	Ala Ala Cys His Gln Pro	Asp Gly Lys Gly		
	405	410	415	
Val Pro Asn Ala Phe Pro	Pro Leu Ala Asn Ser Asp	Tyr Leu Asn Ala		
	420	425	430	
Asp His Ala Arg Ala Ala	Ser Ile Val Ala Asn Gly	Leu Ser Gly Lys		
	435	440	445	
Ile Thr Val Asn Gly Asn	Gln Tyr Glu Ser Val Met	Pro Ala Ile Ala		
	450	455	460	
Leu Ser Asp Gln Gln Ile	Ala Asn Val Ile Thr Tyr	Thr Leu Asn Ser		
465	470	475	480	
Phe Gly Asn Lys Gly Gly	Gln Leu Ser Ala Asp	Asp Val Ala Lys Ala		
	485	490	495	
Lys Lys Thr Lys Pro Asn				
500				

<210> 5  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 5  
 aagcgaacag tttcgccaac c

WO 01/19996

PCT/EP00/09035

<210> 6  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 6  
gggggcgttg actggtgaaa atg

23

<210> 7  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 7  
gtaaaacgac ggccagt

17

<210> 8  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 8  
caggaaacag ctatgac

17

<210> 9  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 9  
acatgtctaa gcctactttg at

22

<210> 10  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 10  
agatctgttt ggcttggttt ttttggc

27